

09/830706

JC08 Rec'd PCT/PTO 27 APR 2001

1/88

SEQUENCE LISTING

<110> Medical & Biological Laboratories Co., Ltd.

<120> Thioredoxin reductase II

<130> M3-007PCT

<140>

<141>

<150> JP 1998-310422

<151> 1998-10-30

<160> 37

<170> PatentIn Ver. 2.0

<210> 1

<211> 1959

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (10).. (1572)

<220>

<221> misc_structure

<222> (1567).. (1569)

<220>

<221> misc_structure

<222> (1664)..(1666)

<223> tga is transrated to selenosysteine, shown by Xaa.

<400> 1

atggcggca atg gcg gtg gcg ctg cgg gga tta gga ggg cgc ttc cgg tgg 51

Met Ala Val Ala Leu Arg Gly Leu Gly Gly Arg Phe Arg Trp

1

5

10

cgg acg cag gcc gtg gcg ggc ggg gtg cgg ggc gcg gcg cgg ggc gca 99

Arg Thr Gln Ala Val Ala Gly Gly Val Arg Gly Ala Ala Arg Gly Ala

15

20

25

30

gca gca ggt cag cgg gac tat gat ctc ctg gtg gtc ggc ggg gga tct 147

Ala Ala Gly Gln Arg Asp Tyr Asp Leu Leu Val Val Gly Gly Gly Ser

35

40

45

ggt ggc ctg gct tgt gcc aag gag gcc gcc cag ctg gga agg aag gtg 195

Gly Gly Leu Ala Cys Ala Lys Glu Ala Ala Gln Leu Gly Arg Lys Val

50

55

60

gcc gtg gtg gac tac gtg gaa cct tct ccc caa ggc acc cgg tgg ggc 243

Ala Val Val Asp Tyr Val Glu Pro Ser Pro Gln Gly Thr Arg Trp Gly

65

70

75

ctc ggc ggc acc tgc gtc aac gtg ggc tgc atc ccc aag aag ctg atg 291

Leu Gly Gly Thr Cys Val Asn Val Gly Cys Ile Pro Lys Lys Leu Met

80

85

90

cac cag gcg gca ctg ctg gga ggc ctg atc caa gat gcc ccc aac tat 339

His Gln Ala Ala Leu Leu Gly Gly Leu Ile Gln Asp Ala Pro Asn Tyr

95

100

105

110

ggc tgg gag gtg gcc cag ccc gtg ccg cat gac tgg agg aag atg gca 387

Gly Trp Glu Val Ala Gln Pro Val Pro His Asp Trp Arg Lys Met Ala

115

120

125

gaa gct gtt caa aat cac gtg aaa tcc ttg aac tgg ggc cac cgt gtc 435
 Glu Ala Val Gln Asn His Val Lys Ser Leu Asn Trp Gly His Arg Val

130

135

140

cag ctt cag gac aga aaa gtc aag tac ttt aac atc aaa gcc agc ttt 483
 Gln Leu Gln Asp Arg Lys Val Lys Tyr Phe Asn Ile Lys Ala Ser Phe

145

150

155

gtt gac gag cac acg gtt tgc ggc gtt gcc aaa ggt ggg aaa gag att 531
 Val Asp Glu His Thr Val Cys Gly Val Ala Lys Gly Gly Lys Glu Ile

160

165

170

ctg ctg tca gcc gat cac atc atc att gct act gga ggg cgg ccg aga 579
 Leu Leu Ser Ala Asp His Ile Ile Ile Ala Thr Gly Gly Arg Pro Arg
 175 180 185 190

tac ccc acg cac atc gaa ggt gcc ttg gaa tat gga atc aca agt gat 627
 Tyr Pro Thr His Ile Glu Gly Ala Leu Glu Tyr Gly Ile Thr Ser Asp
 195 200 205

gac atc ttc tgg ctg aag gaa tcc cct gga aaa acg ttg gtg gtc ggg 675
 Asp Ile Phe Trp Leu Lys Glu Ser Pro Gly Lys Thr Leu Val Val Gly
 210 215 220

gcc agc tat gtg gcc ctg gag tgt gct ggc ttc ctc acc ggg att ggg 723
 Ala Ser Tyr Val Ala Leu Glu Cys Ala Gly Phe Leu Thr Gly Ile Gly
 225 230 235

ctg gac acc acc atc atg atg cgc agc atc ccc ctc cgc ggc ttc gac 771
 Leu Asp Thr Thr Ile Met Met Arg Ser Ile Pro Leu Arg Gly Phe Asp
 240 245 250

cag caa atg tcc tcc atg gtc ata gag cac atg gca tct cat ggc acc 819
 Gln Gln Met Ser Ser Met Val Ile Glu His Met Ala Ser His Gly Thr
 255 260 265 270

cgg ttc ctg agg ggc tgt gcc ccc tcg cgg gtc agg agg ctc cct gat 867
 Arg Phe Leu Arg Gly Cys Ala Pro Ser Arg Val Arg Arg Leu Pro Asp
 275 280 285

ggc cag ctg cag gtc acc tgg gag gac agc acc acc ggc aag gag gac 915
 Gly Gln Leu Gln Val Thr Trp Glu Asp Ser Thr Thr Gly Lys Glu Asp
 290 295 300

acg ggc acc ttt gac acc gtc ctg tgg gcc ata ggt cga gtc cca gac 963
 Thr Gly Thr Phe Asp Thr Val Leu Trp Ala Ile Gly Arg Val Pro Asp
 305 310 315

acc aga agt ctg aat ttg gag aag gct ggg gta gat act agc ccc gac 1011
 Thr Arg Ser Leu Asn Leu Glu Lys Ala Gly Val Asp Thr Ser Pro Asp
 320 325 330

act cag aag atc ctg gtg gac tcc cgg gaa gcc acc tct gtg ccc cac 1059
 Thr Gln Lys Ile Leu Val Asp Ser Arg Glu Ala Thr Ser Val Pro His
 335 340 345 350

atc tac gcc att ggt gac gtg gtg gag ggg cgg cct gag ctg aca ccc 1107
 Ile Tyr Ala Ile Gly Asp Val Val Glu Gly Arg Pro Glu Leu Thr Pro
 355 360 365

aca gcg atc atg gcc ggg agg ctc ctg gtg cag cgg ctc ttc ggc ggg 1155
 Thr Ala Ile Met Ala Gly Arg Leu Leu Val Gln Arg Leu Phe Gly Gly
 370 375 380

tcc tca gat ctg atg gac tac gac aat gtt ccc acg acc gtc ttc acc 1203
 Ser Ser Asp Leu Met Asp Tyr Asp Asn Val Pro Thr Thr Val Phe Thr
 385 390 395

cca ctg gag tat ggc tgt gtg ggg ctg tcc gag gag gag gca gtg gct 1251
 Pro Leu Glu Tyr Gly Cys Val Gly Leu Ser Glu Glu Glu Ala Val Ala
 400 405 410

cgc cac ggg cag gag cat gtt gag gtc tat cac gcc cat tat aaa cca 1299
 Arg His Gly Gln Glu His Val Glu Val Tyr His Ala His Tyr Lys Pro
 415 420 425 430

ctg gag ttc acg gtg gct gga cga gat gca tcc cag tgt tat gta aag 1347
 Leu Glu Phe Thr Val Ala Gly Arg Asp Ala Ser Gln Cys Tyr Val Lys
 435 440 445

atg gtg tgc ctg agg gag ccc cca cag ctg gtg ctg ggc ctg cat ttc 1395
 Met Val Cys Leu Arg Glu Pro Pro Gln Leu Val Leu Gly Leu His Phe
 450 455 460

ctt ggc ccc aac gca ggc gaa gtt act caa gga ttt gct ctg ggg atc 1443
 Leu Gly Pro Asn Ala Gly Glu Val Thr Gln Gly Phe Ala Leu Gly Ile
 465 470 475

aag tgt ggg gct tcc tat gcg cag gtg atg cgg acc gtg ggt atc cat 1491
 Lys Cys Gly Ala Ser Tyr Ala Gln Val Met Arg Thr Val Gly Ile His
 480 485 490

ccc aca tgc tct gag gag gta gtc aag ctg cgc atc tcc aag cgc tca 1539
 Pro Thr Cys Ser Glu Glu Val Val Lys Leu Arg Ile Ser Lys Arg Ser
 495 500 505 510

ggc ctg gac ccc acg gtg aca ggc tgc tga ggg taagcgccat ccctgcaggc 1592
 Gly Leu Asp Pro Thr Val Thr Gly Cys Xaa Gly
 515 520

cagggcacac ggtgcgcccg ccgccagctc ctgcgaggcc agaccagga tggctgcagg 1652

ccaggttttg ggggcctcaa ccctctcctg gagcgctgt gagatggtca gcgtggagcg 1712

caagtgttg acgggtggcc cgtgtgcccc acagggatgg ctgaggggac tgtccacctc 1772

accctgcac ctttcagcct ttgccgccgg gcaccccccc caggctcctg gtgccggatg 1832

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atgacgacct ggggtggaac ctaccctgtg ggcacccatg tccgagcccc ctggcatttc 1892

tgcaatgcaa ataaagaggg tactttttct gaagtgtgta aaaaaaaaaa aaaaaaaaaa 1952

aaaaaaaa 1959

<210> 2

<211> 521

<212> PRT

<213> Homo sapiens

<223> Xaa(520) means selenosysteine.

<400> 2

Met Ala Val Ala Leu Arg Gly Leu Gly Gly Arg Phe Arg Trp Arg Thr

1 5 10 15

Gln Ala Val Ala Gly Gly Val Arg Gly Ala Ala Arg Gly Ala Ala Ala

20 25 30

Gly Gln Arg Asp Tyr Asp Leu Leu Val Val Gly Gly Gly Ser Gly Gly

35 40 45

Leu Ala Cys Ala Lys Glu Ala Ala Gln Leu Gly Arg Lys Val Ala Val

50 55 60

Val Asp Tyr Val Glu Pro Ser Pro Gln Gly Thr Arg Trp Gly Leu Gly

65 70 75 80

Gly Thr Cys Val Asn Val Gly Cys Ile Pro Lys Lys Leu Met His Gln

85 90 95

Ala Ala Leu Leu Gly Gly Leu Ile Gln Asp Ala Pro Asn Tyr Gly Trp

100 105 110

Glu Val Ala Gln Pro Val Pro His Asp Trp Arg Lys Met Ala Glu Ala

7/88

115	120	125
Val Gln Asn His Val Lys Ser Leu Asn Trp Gly His Arg Val Gln Leu		
130	135	140
Gln Asp Arg Lys Val Lys Tyr Phe Asn Ile Lys Ala Ser Phe Val Asp		
145	150	155
160		
Glu His Thr Val Cys Gly Val Ala Lys Gly Gly Lys Glu Ile Leu Leu		
165	170	175
Ser Ala Asp His Ile Ile Ile Ala Thr Gly Gly Arg Pro Arg Tyr Pro		
180	185	190
Thr His Ile Glu Gly Ala Leu Glu Tyr Gly Ile Thr Ser Asp Asp Ile		
195	200	205
Phe Trp Leu Lys Glu Ser Pro Gly Lys Thr Leu Val Val Gly Ala Ser		
210	215	220
Tyr Val Ala Leu Glu Cys Ala Gly Phe Leu Thr Gly Ile Gly Leu Asp		
225	230	235
240		
Thr Thr Ile Met Met Arg Ser Ile Pro Leu Arg Gly Phe Asp Gln Gln		
245	250	255
Met Ser Ser Met Val Ile Glu His Met Ala Ser His Gly Thr Arg Phe		
260	265	270
Leu Arg Gly Cys Ala Pro Ser Arg Val Arg Arg Leu Pro Asp Gly Gln		
275	280	285
Leu Gln Val Thr Trp Glu Asp Ser Thr Thr Gly Lys Glu Asp Thr Gly		
290	295	300
Thr Phe Asp Thr Val Leu Trp Ala Ile Gly Arg Val Pro Asp Thr Arg		

8/88

305 310 315 320

Ser Leu Asn Leu Glu Lys Ala Gly Val Asp Thr Ser Pro Asp Thr Gln
325 330 335

Lys Ile Leu Val Asp Ser Arg Glu Ala Thr Ser Val Pro His Ile Tyr
340 345 350

Ala Ile Gly Asp Val Val Glu Gly Arg Pro Glu Leu Thr Pro Thr Ala
355 360 365

Ile Met Ala Gly Arg Leu Leu Val Gln Arg Leu Phe Gly Gly Ser Ser
370 375 380

Asp Leu Met Asp Tyr Asp Asn Val Pro Thr Thr Val Phe Thr Pro Leu
385 390 395 400

Glu Tyr Gly Cys Val Gly Leu Ser Glu Glu Glu Ala Val Ala Arg His
405 410 415

Gly Gln Glu His Val Glu Val Tyr His Ala His Tyr Lys Pro Leu Glu
420 425 430

Phe Thr Val Ala Gly Arg Asp Ala Ser Gln Cys Tyr Val Lys Met Val
435 440 445

Cys Leu Arg Glu Pro Pro Gln Leu Val Leu Gly Leu His Phe Leu Gly
450 455 460

Pro Asn Ala Gly Glu Val Thr Gln Gly Phe Ala Leu Gly Ile Lys Cys
465 470 475 480

Gly Ala Ser Tyr Ala Gln Val Met Arg Thr Val Gly Ile His Pro Thr
485 490 495

Cys Ser Glu Glu Val Val Lys Leu Arg Ile Ser Lys Arg Ser Gly Leu

9/88

500

505

510

Asp Pro Thr Val Thr Gly Cys Xaa Gly

515

520

<210> 3

<211> 2056

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (188)..(1669)

<223> tga(1664)..(1666) is transrated to selenosysteine, shown by Xaa.

<400> 3

gtcccgacc tcaggcccag ttcagtgtac ttccctctc tacttctcc ctccagtc 60

ttctccatcc ctcccttttt tggtgcccc ttgcctgcct tcctgccag tagcttcag 120

agtagacacg atgacacctt ttgcaggcta aaaaggctga gaggggcact atgtgcagt 180

agccacc atg gag gac caa gca ggt cag cgg gac tat gat ctc ctg gtg 229

Met Glu Asp Gln Ala Gly Gln Arg Asp Tyr Asp Leu Leu Val

1

5

10

gtc ggc ggg gga tct ggt ggc ctg gct tgt gcc aag gag gcc gcc cag 277

Val Gly Gly Gly Ser Gly Gly Leu Ala Cys Ala Lys Glu Ala Ala Gln

15

20

25

30

ctg gga agg aag gtg gcc gtg gtg gac tac gtg gaa cct tct ccc caa 325

Leu Gly Arg Lys Val Ala Val Val Asp Tyr Val Glu Pro Ser Pro Gln

35

40

45

ggc acc cgg tgg ggc ctc ggc ggc acc tgc gtc aac gtg ggc tgc atc 373

10/88

Gly Thr Arg Trp Gly Leu Gly Gly Thr Cys Val Asn Val Gly Cys Ile
50 55 60

ccc aag aag ctg atg cac cag gcg gca ctg ctg gga ggc ctg atc caa 421
Pro Lys Lys Leu Met His Gln Ala Ala Leu Leu Gly Gly Leu Ile Gln
65 70 75

gat gcc ccc aac tat ggc tgg gag gtg gcc cag ccc gtg ccg cat gac 469
Asp Ala Pro Asn Tyr Gly Trp Glu Val Ala Gln Pro Val Pro His Asp
80 85 90

~~tgg agg aag atg gca gaa gct gtt caa aat cac gtg aaa tcc ttg aac 517~~
Trp Arg Lys Met Ala Glu Ala Val Gln Asn His Val Lys Ser Leu Asn
95 100 105 110

tgg ggc cac cgt gtc cag ctt cag gac aga aaa gtc aag tac ttt aac 565
Trp Gly His Arg Val Gln Leu Gln Asp Arg Lys Val Lys Tyr Phe Asn
115 120 125

atc aaa gcc agc ttt gtt gac gag cac acg gtt tgc ggc gtt gcc aaa 613
Ile Lys Ala Ser Phe Val Asp Glu His Thr Val Cys Gly Val Ala Lys
130 135 140

ggt ggg aaa gag att ctg ctg tca gcc gat cac atc atc att gct act 661
Gly Gly Lys Glu Ile Leu Leu Ser Ala Asp His Ile Ile Ile Ala Thr
145 150 155

gga ggg cgg ccg aga tac ccc acg cac atc gaa ggt gcc ttg gaa tat 709
Gly Gly Arg Pro Arg Tyr Pro Thr His Ile Glu Gly Ala Leu Glu Tyr
160 165 170

gga atc aca agt gat gac atc ttc tgg ctg aag gaa tcc cct gga aaa 757
Gly Ile Thr Ser Asp Asp Ile Phe Trp Leu Lys Glu Ser Pro Gly Lys
175 180 185 190

acg ttg gtg gtc ggg gcc agc tat gtg gcc ctg gag tgt gct ggc ttc 805

11/88

Thr Leu Val Val Gly Ala Ser Tyr Val Ala Leu Glu Cys Ala Gly Phe
195 200 205

ctc acc ggg att ggg ctg gac acc acc atc atg atg cgc agc atc ccc 853
Leu Thr Gly Ile Gly Leu Asp Thr Thr Ile Met Met Arg Ser Ile Pro
210 215 220

ctc cgc ggc ttc gac cag caa atg tcc tcc atg gtc ata gag cac atg 901
Leu Arg Gly Phe Asp Gln Gln Met Ser Ser Met Val Ile Glu His Met
225 230 235

~~gca tct cat ggc acc cgg ttc ctg agg ggc tgt gcc ccc tcg cgg gtc 949~~
Ala Ser His Gly Thr Arg Phe Leu Arg Gly Cys Ala Pro Ser Arg Val
240 245 250

agg agg ctc cct gat ggc cag ctg cag gtc acc tgg gag gac agc acc 997
Arg Arg Leu Pro Asp Gly Gln Leu Gln Val Thr Trp Glu Asp Ser Thr
255 260 265 270

acc ggc aag gag gac acg ggc acc ttt gac acc gtc ctg tgg gcc ata 1045
Thr Gly Lys Glu Asp Thr Gly Thr Phe Asp Thr Val Leu Trp Ala Ile
275 280 285

ggc cga gtc cca gac acc aga agt ctg aat ttg gag aag gct ggg gta 1093
Gly Arg Val Pro Asp Thr Arg Ser Leu Asn Leu Glu Lys Ala Gly Val
290 295 300

gat act agc ccc gac act cag aag atc ctg gtg gac tcc cgg gaa gcc 1141
Asp Thr Ser Pro Asp Thr Gln Lys Ile Leu Val Asp Ser Arg Glu Ala
305 310 315

acc tct gtg ccc cac atc tac gcc att ggt gac gtg gtg gag ggg cgg 1189
Thr Ser Val Pro His Ile Tyr Ala Ile Gly Asp Val Val Glu Gly Arg
320 325 330

cct gag ctg aca ccc aca gcg atc atg gcc ggg agg ctc ctg gtg cag 1237

12/88

Pro Glu Leu Thr Pro Thr Ala Ile Met Ala Gly Arg Leu Leu Val Gln
335 340 345 350

cgg ctc ttc ggc ggg tcc tca gat ctg atg gac tac gac aat gtt ccc 1285
Arg Leu Phe Gly Gly Ser Ser Asp Leu Met Asp Tyr Asp Asn Val Pro
355 360 365

acg acc gtc ttc acc cca ctg gag tat ggc tgt gtg ggg ctg tcc gag 1333
Thr Thr Val Phe Thr Pro Leu Glu Tyr Gly Cys Val Gly Leu Ser Glu
370 375 380

~~gag gag gca gtg gct cgc cac ggg cag gag cat gtt gag gtc tat cac 1381~~
Glu Glu Ala Val Ala Arg His Gly Gln Glu His Val Glu Val Tyr His
385 390 395

gcc cat tat aaa cca ctg gag ttc acg gtg gct gga cga gat gca tcc 1429
Ala His Tyr Lys Pro Leu Glu Phe Thr Val Ala Gly Arg Asp Ala Ser
400 405 410

cag tgt tat gta aag atg gtg tgc ctg agg gag ccc cca cag ctg gtg 1477
Gln Cys Tyr Val Lys Met Val Cys Leu Arg Glu Pro Pro Gln Leu Val
415 420 425 430

ctg ggc ctg cat ttc ctt ggc ccc aac gca ggc gaa gtt act caa gga 1525
Leu Gly Leu His Phe Leu Gly Pro Asn Ala Gly Glu Val Thr Gln Gly
435 440 445

ttt gct ctg ggg atc aag tgt ggg gct tcc tat gcg cag gtg atg cgg 1573
Phe Ala Leu Gly Ile Lys Cys Gly Ala Ser Tyr Ala Gln Val Met Arg
450 455 460

acc gtg ggt atc cat ccc aca tgc tct gag gag gta gtc aag ctg cgc 1621
Thr Val Gly Ile His Pro Thr Cys Ser Glu Glu Val Val Lys Leu Arg
465 470 475

atc tcc aag cgc tca ggc ctg gac ccc acg gtg aca ggc tgc tga ggg 1669

13/88

Ile Ser Lys Arg Ser Gly Leu Asp Pro Thr Val Thr Gly Cys Xaa Gly

480

485

490

taagcgccat ccctgcaggc cagggcacac ggtgcgcccg ccgccagctc ctcggaggcc 1729

agaccagga tggctgcagg ccaggtttgg ggggcctcaa ccctctcctg gagcgctgt 1789

gagatggtca gcgtggagcg caagtgtgg acgggtggcc cgtgtgcccc acagggatgg 1849

ctcaggggac tgtccacctc acccctgcac ctttcagcct ttgccgccgg gcaccccccc 1909

~~caggctcctg gtgccgatg atgacgacct ggggtgaaac ctaccctgtg ggcacccatg 1969~~

tccgagcccc ctggcatttc tgcaatgcaa ataaagaggg tactttttct gaagtgtgta 2029

aaaaaaaaa aaaaaaaaaa aaaaaaa

2056

<210> 4

<211> 492

<212> PRT

<213> Homo sapiens

<223> Xaa(493) means selenosysteine.

<400> 4

Met Glu Asp Gln Ala Gly Gln Arg Asp Tyr Asp Leu Leu Val Val Gly

1

5

10

15

Gly Gly Ser Gly Gly Leu Ala Cys Ala Lys Glu Ala Ala Gln Leu Gly

20

25

30

Arg Lys Val Ala Val Val Asp Tyr Val Glu Pro Ser Pro Gln Gly Thr

35

40

45

Arg Trp Gly Leu Gly Gly Thr Cys Val Asn Val Gly Cys Ile Pro Lys

50

55

60

14/88

Lys Leu Met His Gln Ala Ala Leu Leu Gly Gly Leu Ile Gln Asp Ala
65 70 75 80

Pro Asn Tyr Gly Trp Glu Val Ala Gln Pro Val Pro His Asp Trp Arg
85 90 95

Lys Met Ala Glu Ala Val Gln Asn His Val Lys Ser Leu Asn Trp Gly
100 105 110

His Arg Val Gln Leu Gln Asp Arg Lys Val Lys Tyr Phe Asn Ile Lys
115 120 125

Ala Ser Phe Val Asp Glu His Thr Val Cys Gly Val Ala Lys Gly Gly
130 135 140

Lys Glu Ile Leu Leu Ser Ala Asp His Ile Ile Ile Ala Thr Gly Gly
145 150 155 160

Arg Pro Arg Tyr Pro Thr His Ile Glu Gly Ala Leu Glu Tyr Gly Ile
165 170 175

Thr Ser Asp Asp Ile Phe Trp Leu Lys Glu Ser Pro Gly Lys Thr Leu
180 185 190

Val Val Gly Ala Ser Tyr Val Ala Leu Glu Cys Ala Gly Phe Leu Thr
195 200 205

Gly Ile Gly Leu Asp Thr Thr Ile Met Met Arg Ser Ile Pro Leu Arg
210 215 220

Gly Phe Asp Gln Gln Met Ser Ser Met Val Ile Glu His Met Ala Ser
225 230 235 240

His Gly Thr Arg Phe Leu Arg Gly Cys Ala Pro Ser Arg Val Arg Arg
245 250 255

15/88

Leu Pro Asp Gly Gln Leu Gln Val Thr Trp Glu Asp Ser Thr Thr Gly
260 265 270

Lys Glu Asp Thr Gly Thr Phe Asp Thr Val Leu Trp Ala Ile Gly Arg
275 280 285

Val Pro Asp Thr Arg Ser Leu Asn Leu Glu Lys Ala Gly Val Asp Thr
290 295 300

Ser Pro Asp Thr Gln Lys Ile Leu Val Asp Ser Arg Glu Ala Thr Ser
305 310 315 320

Val Pro His Ile Tyr Ala Ile Gly Asp Val Val Glu Gly Arg Pro Glu
325 330 335

Leu Thr Pro Thr Ala Ile Met Ala Gly Arg Leu Leu Val Gln Arg Leu
340 345 350

Phe Gly Gly Ser Ser Asp Leu Met Asp Tyr Asp Asn Val Pro Thr Thr
355 360 365

Val Phe Thr Pro Leu Glu Tyr Gly Cys Val Gly Leu Ser Glu Glu Glu
370 375 380

Ala Val Ala Arg His Gly Gln Glu His Val Glu Val Tyr His Ala His
385 390 395 400

Tyr Lys Pro Leu Glu Phe Thr Val Ala Gly Arg Asp Ala Ser Gln Cys
405 410 415

Tyr Val Lys Met Val Cys Leu Arg Glu Pro Pro Gln Leu Val Leu Gly
420 425 430

Leu His Phe Leu Gly Pro Asn Ala Gly Glu Val Thr Gln Gly Phe Ala
435 440 445

16/88

Leu Gly Ile Lys Cys Gly Ala Ser Tyr Ala Gln Val Met Arg Thr Val

450

455

460

Gly Ile His Pro Thr Cys Ser Glu Glu Val Val Lys Leu Arg Ile Ser

465

470

475

480

Lys Arg Ser Gly Leu Asp Pro Thr Val Thr Gly Cys Xaa Gly

485

490

<210> 5

<211> 130

<212> DNA

<213> Homo sapiens

<400> 5

tcagcctttg ccgccgggca cccccccag gctcctgggtg ccgatgatg acgacctggg 60

tggaacctta ccctgtgggc acccatgtcc gagccccctg gcatttctgc aatgcaaata 120

aagagggtac

130

<210> 6

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthesis

<400> 6

gcgggatcca tgacttttaa cagttttgaa gg

32

<210> 7

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthesis

<400> 7

gcgctcgagc tactatagag ttagattaag ac

32

<210> 8

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthesis

<400> 8

tatgatctcc tgggtggtc

18

<210> 9

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthesis

<400> 9

gtcatcactt gtgattcc

18

<210> 10

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthesis

<400> 10

acagcttctg ccattcttcct c

21

<210> 11

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthesis

<400> 11

agaaggttcc acgtagtcca c

21

<210> 12

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthesis

<400> 12

ccatacgatg ttccagatta c

21

<210> 13
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:synthesis

<400> 13
 acgatggcgg caatggcggg g 21

<210> 14
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:synthesis

<400> 14
 accatggagg accaagcagg t 21

<210> 15
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:synthesis

<400> 15
 ttaccctcag cagcctgtca c 21

<210> 16

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthesis

<400> 16

gcgccatccc tgcaggccag g

21

<210> 17

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthesis

<400> 17

cacacttcag aaaaagtacc c

21

<210> 18

<211> 103

<212> DNA

<213> Homo sapiens

<400> 18

atggcggcaa tggcgggtggc gctgcgggga ttaggagggc gcttccggtg gcggacgcag 60

gccgtggcgg gcgggggtgcg gggcgcggcg cggggcgcag cag

103

<210> 19

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<211> 200

<212> DNA

<213> Homo sapiens

<400> 19

gtcccggacc tcaggcccag ttcagtgtac ttccctctc tacttcctcc ctccagtccc 60

ttctccatcc ctcccttttt tggtgcccc ttgcctgcct tcctgccag tagcttgag 120

agtagacacg atgacacctt ttgcaggcta aaaaggctga gaggggcact atgtgcagt 180

agccaccatg gaggaccaag 200

<210> 20

<211> 69

<212> DNA

<213> Homo sapiens

<400> 20

caggtcagcg ggactatgat ctctgggtgg tggcggggg atctgggtggc ctggcttggtg 60

ccaaggagg 69

<210> 21

<211> 57

<212> DNA

<213> Homo sapiens

<400> 21

ccgccagct gggaaggaag gtggtggtgg tggactacgt ggaaccttct cccaag 57

<210> 22

<211> 145

22/88

<212> DNA

<213> Homo sapiens

<400> 22

gcacccggtg gggcctcggc ggcacctgcg tcaacgtggg ctgcatcccc aagaagctga 60

tgcaccaggc ggcactgctg ggaggcctga tccaagatgc cccaactat ggctgggagg 120

tgccccagcc cgtgccgcat gactg 145

<210> 23

<211> 75

<212> DNA

<213> Homo sapiens

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